Amendments to the Specification

Please amend paragraph [0114] appearing on page 54 of the specification as follows:

It has been reported that tyrosine kinase inhibitors, such as STI571 (Imatinib mesilate, ~~Gleevec~~ GLEEVEC®), have potent synergetic effect in combination with other anti-leukemic agents, such as etoposide (Liu, W.M., *et al. Br. J. Cancer 86*:1472-1478 (2002)). Therefore, another embodiment of the present invention is directed to compositions and methods effective to inhibit neoplasia comprising an AIP binding compound, or a pharmaceutically acceptable salt or prodrug of an AIP binding compound described herein, which functions as a caspase cascade activator and inducer of apoptosis, in combination with at least one known tyrosine kinase inhibitor, or a pharmaceutically acceptable salt of the agent. Examples of known tyrosine kinase inhibitors, which can be used for combination therapy include, but are not limited to, ~~gleevec~~ GLEEVEC®, ZD1839 (~~Iressa~~ IRESSA®), SH268, genistein, CEP2563, SU6668, SU11248, and EMD121974.

Please amend paragraph [0118], appearing on page 56 of the specification as follows:

It has been reported in clinical studies that regular administration of non-steroidal anti-inflammatory drugs (NSAIDs) reduces the risk of breast cancer. ~~*See* Study: Why aspirin, fiber prevent cancer, posted Wenesday, April 9, 2003 at http://www.cnn.com/2003/Health/04/09/health.cancer.aspirin.reut/index.html.~~ It has also been reported that in colon cancer cells, NSAIDs prevent interleukin-6 from activating STAT1; STAT1 prevents cellular suicide. ~~*Id.*~~ Hence, NSAIDs are believed to make cells more conducive to apoptosis. Therefore, another embodiment of the present invention is directed to compositions and methods effective to inhibit neoplasia comprising an AIP binding compound, or a pharmaceutically acceptable salt or prodrug of an AIP binding compound described herein, which functions as a caspase cascade

activator and inducer of apoptosis, in combination with at least one known NSAID, or a pharmaceutically acceptable salt of the agent. Examples of known NSAIDs, which can be used for combination therapy include, but are not limited to, ibuprofen, aspirin and sulindac.

Please amend paragraph [0308], appearing on page 156 of the specification as follows[1]:

An NCBI Blast search ~~(accessible at http://www.ncbi.nlm.nih.gov/BLAST/)~~ using this peptide revealed that it is a part of SEQ ID NO: 1 or 4.

Sequence	aa Positions
VSASPLLYTLIEK	amino acids 496-508 of SEQ ID NO. : 1 or 4

EXAMPLE 34

Isolation and Identification of Transferrin Receptor

Isolation of transferrin receptor from plasma membrane fraction of Jurkat cells by gambogyl affinity chromatography:

Please amend paragraph [0315], appearing on pages 159-160 of the specification as follows:

The following lists the experimentally deduced peptide sequences having the closest fitting calculated molecular weights. An NCBI Blast search ~~(accessible at http://www.ncbi.nlm.nih.gov/BLAST/)~~ using these peptides revealed that they are a part of SEQ ID NO: 1 or 4.

[1] Underlining of "Sequence" and "aa Positions" is as it appears in the original.

Sequence:	aa positions
AVLGTSNFK	amino acids 487-495 of SEQ ID NO.: 1 or 4
GFVEPDHYVVVGAQR	amino acids 395-409 of SEQ ID NO.: 1 or 4
ILNIFGVIK	amino acids 386-394 of SEQ ID NO.: 1 or 4
LAVDEEENADNNTK	amino acids 40-53 of SEQ ID NO.: 1 or 4
LLNENSYVPR	amino acids 146-155 of SEQ ID NO.: 1 or 4
LTTDFGNAEK	amino acids 656-665 of SEQ ID NO.: 1 or 4
LVYLVENPGGYVAYSK	amino acids 209-224 of SEQ ID NO.: 1 or 4
SAFSNLFGGEPLSYTR	amino acids 7-22 of SEQ ID NO.: 1 or 4
SSGLPNIPVQTISR	amino acids 326-339 of SEQ ID NO.: 1 or 4
VSASPLLYTLIEK	amino acids 496-508 of SEQ ID NO.: 1 or 4

EXAMPLE 35

Immunofluorescence, Immunohistochemistry, and Electron Microscopy

Please amend paragraph [0340], appearing on pages 170-171 of the specification as follows:

The following table lists the experimentally determined molecular weights, Mr(expt), of the column fractions, and peptides having the closest fitting calculated molecular weight, Mr(calc). The difference between Mr(expt) and Mr(calc) is indicated

as "Delta." An NCBI Blast search ~~(accessible at http://www.ncbi.nlm.nih.gov/BLAST/)~~ using these peptides revealed that they are a part of SEQ ID NO: 34. Query refers to the sample number, Observed is the m/z ratio, Mr(expt) is the experimental mass adjusted for charge, Mr(calc) is the predicted peptide mass, Delta is the difference between the experimental and calculated mass, and Peptide is the amino acid sequence.

Please amend paragraph [0345], appearing on pages 175-176 of the specification:

The following table lists the experimentally determined molecular weights, Mr(expt), of the column fractions, and peptides having the closest fitting calculated molecular weight, Mr(calc). The difference between Mr(expt) and Mr(calc) is indicated as "Delta." An NCBI Blast search ~~(accessible at http://www.ncbi.nlm.nih.gov/BLAST/)~~ using these peptides revealed that they are a part of SEQ ID NO: 36. Query refers to the sample number, Observed is the m/z ratio, Mr(expt) is the experimental mass adjusted for charge, Mr(calc) is the predicted peptide mass, Delta is the difference between the experimental and calculated mass, and Peptide is the amino acid sequence.

Query	Observed	Mr(expt)	Mr(calc)	Delta	Peptide
225	465.51	929.00	930.50	-1.50	TALQEEIK (amino acids 1028-1035 of SEQ ID NO.: 36)
254	508.23	1014.44	1014.49	-0.05	MLQHAASNK+Oxidation (M) (amino acids 1231-1239 of SEQ ID NO.: 36)
287	547.15	1092.28	1092.48	-0.19	LTAEEMDER (amino acids 26-34 of SEQ ID NO.: 36)
312	589.01	1176.00	1175.57	0.44	EDSNLTLQEK (amino acids 1446-1455 of SEQ ID NO.: 36)
331	617.58	1233.14	1232.59	0.55	FPDAGEDELLK (amino acids 1175-1185 of SEQ ID NO.: 36)
502	735.11	1468.20	1467.66	0.55	VDFTEEEINNMK (amino acids 175-186 of SEQ ID NO.: 36)
508	742.83	1483.64	1483.65	-0.01	VDFTEEEINNMK

					+Oxidation (M) (amino acids 175-186 of SEQ ID NO.: 36)
509	745.88	1489.74	1489.76	-0.02	SVKEDSNLTLQEK (amino acids 1443-1455 of SEQ ID NO.: 36)
535	783.23	1564.44	1564.65	-0.20	FDVPGDENAEMDAR (amino acids 1369-1382 of SEQ ID NO.: 36)
539	791.27	1580.52	1580.64	-0.12	FDVPGDENAEMDAR +Oxidation (M) (amino acids 1369-1382 of SEQ ID NO.: 36)
561	544.15	1629.43	1628.72	0.71	NKEQLSDMMMINK +3 Oxidation (M) (amino acids 941-953 of SEQ ID NO.: 36)

EXAMPLE 43

Isolation and Identification of Heat Shock Protein

Isolation of heat shock protein from plasma membrane fraction of Jurkat cells by gambogyl affinity chromatography:

Please amend paragraph [0352], appearing on page 179 of the specification, as follows:

The following table lists the experimentally deduced peptide sequences having the closest fitting calculated molecular weights. An NCBI Blast search ~~(accessible at http://www.nebi.nlm.nih.gov/BLAST/)~~ using these peptides revealed that they are a part of SEQ ID NO: 38.

Sequence:	aa positions
ADLINNLGTIAK	amino acids 96-107 of SEQ ID NO.: 38
AKFENLCK	amino acids 558-565 of SEQ ID NO.: 38
ALLFIPR	amino acids 331-337 of SEQ ID NO.: 38
ELISNASDALDK	amino acids 42-53 of SEQ ID NO.: 38
ELISNASDALDKIR	amino acids 42-55 of SEQ ID NO.: 38
ELKIDIIPNPQER	amino acids 70-82 of SEQ ID NO.: 38
EQVANSAFVER	amino acids 492-502 of SEQ ID NO.: 38
FYEAFSK	amino acids 429-435 of SEQ ID NO.: 38
GVVDSEDLPLNISR	amino acids 379-392 of SEQ ID NO.: 38
HLEINPDHPIVETLR	amino acids 625-639 of SEQ ID NO.: 38
HSQFIGYPITLYLEK	amino acids 205-219 of SEQ ID NO.: 38
HSQFIGYPITLYLEKER	amino acids 205-221 of SEQ ID NO.: 38
KHLEINPDHPIVETLR	amino acids 624-639 of SEQ ID NO.: 38
KHSQFIGYPITLYLEK	amino acids 204-219 of SEQ ID NO.: 38
NPDDITQEEYGEFYK	amino acids 292-306 of SEQ ID NO.: 38
RAPFDLFENK	amino acids 338-347 of SEQ ID NO.: 38
SIYYITGESK	amino acids 482-491 of SEQ ID NO.: 38
SIYYITGESKEQVANSAFVER	amino acids 482-502 of SEQ ID NO.: 38
SLTNDWEDHLAVK	amino acids 307-319 of SEQ ID NO.: 38
SLVSVTK	amino acids 532-538 of SEQ ID NO.: 38
TLTLVDTGIGMTK	amino acids 83-95 of SEQ ID NO.: 38
YESLTDPSKLDSGK	amino acids 56-69 of SEQ ID NO.: 38
YIDQEELNK	amino acids 276-284 of SEQ ID NO.: 38

Amendments to the Abstract

Please replace the abstract with the following abstract:

The present invention relates to screening methods useful for drug discovery of apoptosis inducing compounds. In particular, the screening methodology relates to using Apoptosis Inducing Proteins (AIPs) as a target for the discovery of apoptosis activators useful as anticancer agents. The screening methods of the present invention can employ homogenous or heterogeneous binding assays using purified or partially purified AIPs; or whole cell assays using cells with altered levels of one or more AIPs. The invention also contemplates use of gambogic acid or GA-related compounds which bind AIPs and can accordingly be used to raise antibodies useful for drug discovery. Alternatively, labeled GA is used for competitive binding assays for drug discovery. Such assays afford high throughput screening of chemical libraries for apoptosis activators.